

SEQUENCE LISTING

<110> Hong Zhang
Andrew T. Watt

<120> ANTISENSE MODULATION OF CASPASE 7 EXPRESSION

<130> RTS-0201

<160> 174

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Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser Ala Asn Glu Asp
5 10 15 20

tca gtg gat gct aag cca gac cgg tcc tcg ttt gta ccg tcc ctc ttc 151
Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val Pro Ser Leu Phe
25 30 35

agt aag aag aag aaa aat gtc acc atg cga tcc atc aag acc acc cgg 199

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Asp	Arg	Val	Pro	Thr	Tyr	Gln	Tyr	Asn	Met	Asn	Phe	Glu	Lys	Leu	Gly	
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Lys	Cys	Ile	Ile	Ile	Asn	Asn	Lys	Asn	Phe	Asp	Lys	Val	Thr	Gly	Met	
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ggc	gtt	cga	aac	gga	aca	gac	aaa	gat	gcc	gag	gcg	ctc	ttc	aag	tgc	343
Gly	Val	Arg	Asn	Gly	Thr	Asp	Lys	Asp	Ala	Glu	Ala	Leu	Phe	Lys	Cys	
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ttc	cga	agc	ctg	ggt	ttt	gac	gtg	att	gtc	tat	aat	gac	tgc	tct	tgt	391
Phe	Arg	Ser	Leu	Gly	Phe	Asp	Val	Ile	Val	Tyr	Asn	Asp	Cys	Ser	Cys	
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gcc	aag	atg	caa	gat	ctg	ctt	aaa	aaa	gct	tct	gaa	gag	gac	cat	aca	439
Ala	Lys	Met	Gln	Asp	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Glu	Asp	His	Thr	
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Asn	Ala	Ala	Cys	Phe	Ala	Cys	Ile	Leu	Leu	Ser	His	Gly	Glu	Glu	Asn	
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His	Phe	Arg	Gly	Asp	Arg	Cys	Lys	Thr	Leu	Leu	Glu	Lys	Pro	Lys	Leu	
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Phe	Phe	Ile	Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Asp	Gly	Ile	Gln	
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gcc	gac	tcg	ggg	ccc	atc	aat	gac	aca	gat	gct	aat	cct	cga	tac	aag	679
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Ile	Pro	Val	Glu	Ala	Asp	Phe	Leu	Phe	Ala	Tyr	Ser	Thr	Val	Pro	Gly	
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Tyr	Tyr	Ser	Trp	Arg	Ser	Pro	Gly	Arg	Gly	Ser	Trp	Phe	Val	Gln	Ala	
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ctc	tgc	tcc	atc	ctg	gag	gag	cac	gga	aaa	gac	ctg	gaa	atc	atg	cag	823
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atc	ctc	acc	agg	gtg	aat	gac	aga	gtt	gcc	agg	cac	ttt	gag	tct	cag	871
Ile	Leu	Thr	Arg	Val	Asn	Asp	Arg	Val	Ala	Arg	His	Phe	Glu	Ser	Gln	
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Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val	
280 285 290	

tcc atg ctc acc aag gaa ctc tac ttc agt caa tag ccatatcagg	965
Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	
295 300	

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tcaaactaat cactcacttt ccctcttcag catagttcaa ccaacagtag cacactttca 180

cctacaaatc ttaaagtagc tccatcaaat ctgcagtttt cacattattg aaaatgtctg 240

tcacataggt acaaatttag aatcatcaca ttatattaca tggctattct aggtcatcta 300

tagatcagat cttagactac agtgattgaa gttcttcgta cagccatcaa aaagggacac 360

atgatcatta cctactgtta gctcacatct aaaggcatga aaaggtttcc tttttttcaa 420

ctgacccaaa cactttaccc caatagtgcc aggttccctc tctgctgctt tga atg 476
Met
1

ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg 524
Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
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ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc 572
Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
20 25 30

gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa 620
Ala Val Gly Thr Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu
35 40 45

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Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg
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tcc tct atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct 716
Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser
70 75 80

gcg ggc ccc gtc agg acc ggc cgg gac cga gtg ccc act tat ctg tac 764
Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr
85 90 95

cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag	812
Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys	
100 105 110	
aac ttc gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa	860
Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys	
115 120 125	
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Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val	
130 135 140 145	
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Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg	
150 155 160	
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Lys Ala Ser Glu Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val	
165 170 175	
ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg	1052
Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val	
180 185 190	
aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa	1100
Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys	
195 200 205	
acc ctg tta gag aaa ccc aaa ctc ttc ttc att cag gca tgc cga ggg	1148
Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly	
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230 235 240	
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245 250 255	
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Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly	
260 265 270	
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275 280 285	
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Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg	
290 295 300 305	
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Val Ala Arg His Phe Glu Ser Gln Ser Asp Asp Pro Arg Phe Asn Glu	
310 315 320	
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325 330 335	

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Phe Ser Arg
340

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 Met Ala Asp Asp Gln Gly Cys Ile Glu
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gag cag ggg gtt gag gat tca gca aat gaa gat tca gtg gat gct aag	461
Glu Gln Gly Val Glu Asp Ser Ala Asn Glu Asp Ser Val Asp Ala Lys	
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Pro Asp Arg Ser Phe Val Pro Ser Leu Phe Ser Lys Lys Lys Lys	
30 35 40	
aat gtc acc atg cga tcc atc aag acc acc cgg gac cga gtg cct aca	557
Asn Val Thr Met Arg Ser Ile Lys Thr Thr Arg Asp Arg Val Pro Thr	
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tat cag tac aac atg aat ttt gaa aag ctg ggc aaa tgc atc ata ata	605
Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly Lys Cys Ile Ile Ile	
60 65 70	
aac aac aag aac ttt gat aaa gtg aca ggt atg ggc gtt cga aac gga	653
Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met Gly Val Arg Asn Gly	
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aca gac aaa gat gcc gag gcg ctc ttc aag tgc ttc cga agc ctg ggt	701
Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys Phe Arg Ser Leu Gly	
90 95 100 105	
ttt gac gtg att gtc tat aat gac tgc tct tgt gcc aag atg caa gat	749
Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys Ala Lys Met Gln Asp	
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ctg ctt aaa aaa gct tct gaa gag gac cat aca aat gcc gcc tgc ttc	797
Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr Asn Ala Ala Cys Phe	
125 130 135	
gcc tgc atc ctc tta agc cat gga gaa gaa aat gta att tat ggg aaa	845
Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn Val Ile Tyr Gly Lys	
140 145 150	
gat ggt gtc aca cca ata aag gat ttg aca gcc cac ttt agg ggg gat	893
Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp	
155 160 165	
aga tgc aaa acc ctt tta gag aaa ccc aaa ctc ttc ttc att cag gct	941
Arg Cys Lys Thr Leu Leu Glu Lys Pro Lys Phe Phe Ile Gln Ala	
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Asp Phe Leu Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg	
220 225 230	
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Ser Pro Gly Arg Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu	
235 240 245	

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Glu Glu His Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val	
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Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln Ser Asp Asp Pro His	
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ttc cat gag aag aag cag atc ccc tgt gtg gtc tcc atg ctc acc aag	1277
Phe His Glu Lys Lys Gln Ile Pro Cys Val Val Ser Met Leu Thr Lys	
285 290 295	
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Glu Leu Tyr Phe Ser Gln	
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2661

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<222> (229)...(1239)

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aaggacaggg aggagaaagt ataaggcctg ctgtaccctc gatgcaaaac atgagaaagc	180
cgactgtgcc agtcccagcc gccctaccgc cgtgggaacg atgctgta atg gac tgt	237
Met Asp Cys	
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gtt ggt tgg cct cca ggc agg aag tgg cac ttg gaa aag aac acc agc	285
Val Gly Trp Pro Pro Gly Arg Lys Trp His Leu Glu Lys Asn Thr Ser	
5 10 15	
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Cys Gly Gly Ser Ser Gly Ile Cys Ala Ser Tyr Val Thr Gln Met Ala	
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Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val Pro Ser	
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Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr	
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Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe Glu Lys	
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Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys Val Thr	
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Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe	
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Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys	
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His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Ser His Gly Glu	
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Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu Lys Pro	
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Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Asp Gly	
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Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu Glu Ile	
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Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly Lys Cys Ile Ile Ile	60		65		70	
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 gtgggaacg atg acc gat gat cag gac tgt gct gcg gag ctg gaa aag gtg 231
 Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu Lys Val
 1 5 10
 gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc tcc tct 279
 Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg Ser Ser
 15 20 25 30
 atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct gcg ggc 327
 Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser Ala Gly
 35 40 45
 ccc gtc agg acc ggc cgg gac cga gtg ccc act tat ctg tac cgc atg 375
 Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr Arg Met
 50 55 60
 gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag aac ttc 423
 Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe
 65 70 75
 gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa gat gca 471
 Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys Asp Ala
 80 85 90

ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta acc gtc Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val Thr Val 95 100 105 110	519
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tccagcgaag acggagttga cgccaagcca gaccgctcct ctatcatctc ctctattctc	180
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cactggtggg gaccgcaggg aggtggcaag tgagggagag gtgcatgggt ggagagaaga	300
ggggcgtcgg caaagcgagg tttgtggagg tccggaatgg gacggagaaa gatgcagggg	360
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